

CTGCAGTCTATTGGATGAAGAGTGTACATATTTCATATAAATCTTAAAGTAGGCAGAAATTAAGG
GGGATGGAAATATATACTTGTACTGCCTTAGATAGTCAACCAGGATGTTGTTACAGTCTTCGTTT
ACTGCTTCTGAAGCCTATACTGATAGAATTAATAAAATACTGAGAGAGAGAGAGAGAGGGACAGAG
AGAGAGAGAGGGGAAGA
GAAGAAAACAAGGTSAGCCATCTGCTTAACTTATGTCCACATTCTCTCAAGAGCATTGTCTTA
TTTGTAGAATTATCTATATTGTTAAGAATCATCTCCATTGTTAAGATTTTGTGGGCTGGAGATC
CAGCTCTGTTGATAAAGTGCTTGCCTAACATGCATGAAGTCCTAGGTTCTATTCCCAAGGCTAC
ATAAAACCTTGTGTTGTGATGAATGCCTGTAATCCCAGTACGCAGCAAGGAGAGACAAGGAGGA
TCAGAAGCTTAAGGACATCATTTTGTACATAGTGAGTTTGAGGAAAGCTGAGGTTACATGGAAC
TCTCTCTCTCTCAAAAACAAAACAAAACAAAACAAAACCTTCTACTAATATTCTGGATTCTGTT
TGATTTTTAGGATCTCAAGAGCATGCTGACGTCATTTATGTGTTTCCATCAGATACAGACAGAG
ATCATAAACATTTAACTCATTGATTATATGTTGAGAGTTGTCCCTCAAGAACCAATGGCCAAAC
ATCCACTGAGGATACACGGAAGCTTAGAAAATCTCTAATTAATAATCCTGACATAATGGAAGTGC
TCACAAACCAGCCAACACCTAATAAAACCAGTGGCAAGAGCAACAACCTCGGCATTTTCTACTT
TGAATCCTGCCAACCCCCCTTTTCTAGCCATACTCTTGCTACTCATAGCATATACTGTGATCCTA
ATCATGGGCATTTTTTGAAACCTCTCTCTTATCATCATCATCTTTAAGAAACAGAGAGAAGCTC
AAAATGTTACCAACATACTGATTGCCAACCTGTCCCTCTCTGACATCTTGGTGTGTGTCATGTG
CATCCCTTTTACGGTCATCTACACTCTGATGGACCACTGGGTATTTGGGAACACTATGTGTAA
CTCACTTCCTACGTGCAAAGTGTCTCAGTTTCTGTGTCCATATTCTCCCTTGTGTTGATTGCTA
TTGAACGATATCAGCTGATTGTGAACCCCGTGGCTGGAAACCAGAGTAGCTCATGCCTATTG
GGGGATCATCTTGATTGCGCTCATTTCTCTGACATTGTCTATTCCCTTATTCCCTGTCTACCAC
CTCACCAATGAGCCCTTTCATAATCTCTCTCTCCCTACTGACATCTACACCCACCAGGTAGCTT
GTGTGGAGATTTGGCCTTCTAAACTGAACCAACTCCTCTTTTCTACATCATTATTTATGCTCCA
GTATTTTGTCCCTCTGGGTTTCATTCTTATCTGCTACCTGAAGATCGTTCTCTGCCTCCGAAAA
AGAACTAGGCAGGTGGACAGGAGAAAGGAAAATAAGAGCCGTCTCAATGAGAACAAGAGGGGTAA
ATGTGATGTTGATTTCCATCGTAGTGACTTTTGGAGCCTGCTGGTTGCCCTTGAACATTTTCAA
TGTCATCTTTCGACTGGTATCATGAGATGCTGATGAGCTGCCACCACGACCTGGTATTTGTAGTT
TGCCACTTGATTGCTATGGTTTCTACTTGCATAAATCCTCTCTTTTATGGATTCTCAACAAAA
ACTTCCAGAAGGATCTAATGATGCTTATTCACCACTGTTGGTGTGGTGAACCTCAGGAAAGTTA
TGAAAATATTGCCATGTCTACTATGCACACAGATGAATCCAAGGGATCATTAAAACTGGCTCAC
ATACCAACAGGCATATAGAACTGGTAAGCAAAATCAAAGCCCTTCTGTTATGAAAGAAAGAGA
AGAAAATAGTATGGAATAGGGCAAGGTGCAGAGGAAGCCAGACTTAAACACATAATATCTTTGGG
CCCAGTTTTGCTTTAAGTTAAGCATGTCTACTCCATTTCAGCCATAGAACACACAGAGATTTATC
CCTACCCTTTCTTTTTTTTCCCTTGGGAAGAATAATAACTTAAACAACCTAGACATCATTACTGAG
GAAGAGAACAAAAATGAGAGAGCATACAAGGACAGCAGAGATGTCTGGGGTACAAAATTCACGT
TATTCGCTGGAATAGCTAGAAAGTTATTAGTTGTGCTGCAG (SEQ ID NO:1)

FIGURE 1

underlined = deleted in targeting construct

[] = sequence flanking Neo insert in targeting construct

[CTGCAGTCTATTGGATGAAGAGTGTACATATTCATATAATTCTTAAAGTAGGCAGAAAT
TAAAGGGGATGGAAATATATACTTGTACTGCCTTAGATAGTCACCAGGATGTTGTTACAG
TCTTCGTTTACTGCTTCTGAAGCCTATACTGATAGAATTAATAAAATACTGAGAGAGAGA
GAGAGGGACAGAGAGAGAGAGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA
GAGAGAGAGAGAGAAGAGAAGAAAACAAGGTTSAAGCCATCTGCTTAACTTATGTCCACAT
TCTCTCAAGAGCATTTGTCTTATTTGTAGAATTATCTATATTGTTAAGAATCATCTCCATT
GTTAAGATTTTGTGGGCTGGAGATCCAGCTCTGTTGATAAAGTGCTTGCCTAACATGCAT
GAAGTCCTAGGTTCTATTCCCAAGGCTACATAAAACCTTGTGTTGTGATGAATGCCTGTA
ATCCCAGTACGCAGCAAGGAGAGACAAGGAGGATCAGAAGCTTAAGGACATCATTTTGTGA
CATAGTGAGTTTGAGGAAAGCTGAGGTTACATGGAACCTCTCTCTCTCTCAAAAACAAAAC
AAAACAAAACAAAACCTTCTACTAATATTCTGGATTCTGTTTGATTTTATAGGATCTCAAG
AGCATGCTGACGTCATTTATGTGTTTCCATCAGATACAGACAGAGATCATAAACATTTAA
CTCATTGATTATATGTTGAGAGTTGTCCCTCAAGAACCAATGGCCAAACATCCACTGAGG
ATACACGGAAGCTTAGAAAATCTCTAATTTAAATCCTGACATAATGGAAGTGCTCACAAA
CCAGCC]AACACCTAATAAAACCAGTGGCAAGAGCAACAACCTCGGCATTTTTCTACTTTG
AATCCTGCCAACCCCTTTTCTAGCCATACTCTTGCTACTCATAGCATATACTGTGATCC
TAATCATGGGCATTTTGGAAACCTCTCTCTTATCATCATCATCTTTAAGAAACAGAGAG
AAGCTCAAAATGTTACCAACATACCTGATT[GCCAACCTGTCCCTCTCTGACATCTTGGTG
TGTGTCATGTGCATCCCTTTTACGGTCATCTACACTCTGATGGACCACTGGGTATTTGGG
AACACTATGTGTAACTCACTTCCTACGTGCAAAGTGCTCAGTTTCTGTGTCCATATTC
TCCCTTGTGTTGATTGCTATTGAACGATATCAGCTGATTGTGAACCCCGTGGCTGGAAA
CCCAGAGTAGCTCATGCCTATTGGGGGATCATCTTGATTTGGCTCATTTCTCTGACATTG
TCTATTCCCTTATTCCCTGTCTTACCACCTACCAATGAGCCCTTTCATAATCTCTCTCTC
CCTACTGACATCTACACCCACCAGGTAGCTTGTGTGGAGATTGGCCTTCTAAACTGAAC
CAACTCCTCTTTTCTACATCATTATTTATGCTCCAGTATTTTGTCCCTCTGGGTTTCATT
CTTATCTGCTACCTGAAGATCGTTCTCTGCCTCCGAAAAAGAACTAGGCAGGTGGACAGG
AGAAAGGAAAAATAAGAGCCGTCTCAATGAGAACAAAGAGGGTAAATGTGATGTTGATTTC
ATCGTAGTGACTTTTGGAGCCTGCTGGTTGCCCTTGAACATTTTCAATGTCATCTTCGAC
TGGTATCATGAGATGCTGATGAGCTGCCACCACGACCTGGTATTTGTAGTTTGCCACTTG
ATTGCTATGGTTTCTACTTGCATAAATCCTCTCTTTTATGGATTCTCAACAAAAACTTC
CAGAAG]GATCTAATGATGCTTATTCACCACTGTTGGTGTGGTGAACCTCAGGAAAGTTA
TGAAAATATTGCCATGTCTACTATGCACACAGATGAATCCAAGGGATCATTTAAACCTGGC
TCACATACCAACAGGCATATAGAAACTGGTAAGCAAAAATCAAAGCCCTTCTGTTATGAAA
GAAAGAGAAGAAATAGTATGGAATAGGGCAAGGTGCAGAGGAAGCCAGACTTAAACACAT
AATATCTTTGGGCCCAGTTTGTCTTAAAGTTAAGCATGTCTACTCCATTGAGCCATAGAA
CACACAGAGATTTATCCCTACCCTTTCTTTTTCCTTTTGAAGAATAATAACTTAAACA
ACCTAGACATCATTACTGAGGAAGAGAACAAAAATGAGAGAGCATACAAGGACAGCAGAG
ATGTCTGGGGTACAAAATTCACGTTATTCGCTGGAATAGCTAGAAAGTTATTAGTTGTGC
TGCAG

FIGURE 2A

Gene Sequence Structure

846 bp

Sequence Deleted

1047 bp

Size of CDS: 2281 bp

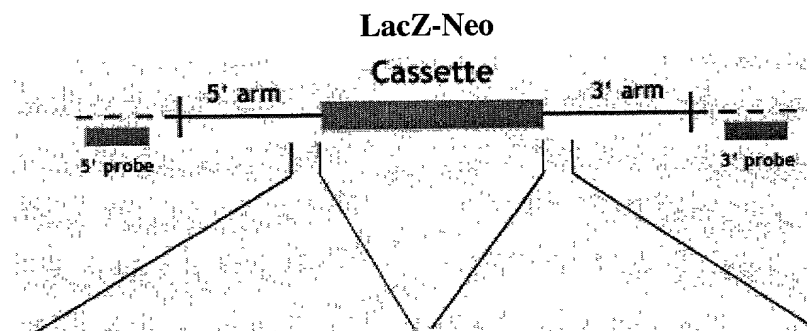
Targeting Vector* (genomic sequence)

Construct Number: 2762

Arm Length:

5': 5 kb

3': 0.5 kb



5' >TTTAGGATCTCAAGAGCATGC
TGACGTCATTTATGTGTTCCATC
AGATACTGACAGAGATCATAAACA
TTTAACTCATTGATTATATGTTGA
GAGTTGTCCCCTCAAGAACCAATGG
CCAAACATCCACTGAGGATACACG
GAAGCTTAGAAAATCTCTAATTAA
AATCCTGACATAATGGAAGTGCTC
ACAAACCAGCC<3'
(SEQ ID NO:2)

5' >GCCAACCTGTCCCTCTCTGAC
ATCTTGGTGTGTGTCATGTGCATC
CCTTTTACGGTCATCTACACTCTG
ATGGACCACTGGGTATTTGGGAAC
ACTATGTGTAAACTCACTTCCTAC
GTGCAAAGTGTCTCAGTTTCTGTG
TCCATATTCTCCCTTGTGTTGATT
GCTATTGAACGATATCAGCTGATT
GTGAACCCCG<3'
(SEQ ID NO:3)

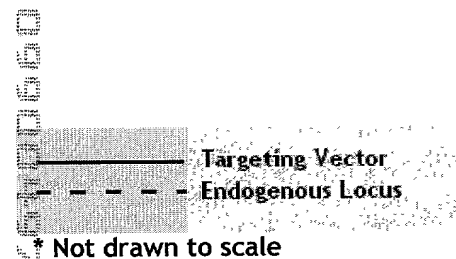


FIGURE 2B